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Scientific and Technical Information Center

SEARCH REQUEST FORM

Requester's Full Name: JANE ZARA Examiner #: 77512 Date: 5-17-95
Art Unit: 1635 Phone Number: 2-076 Serial Number: 0914867757
Location (Bldg/Room#): 2D28 (Mailbox #): 218 Results Format Preferred (circle): PAPER DISK

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: Cytochrome P-450 reductase
Inventors (please provide full names): KUTCHAN et al.

Earliest Priority Date: 7/13/00 CRF

Search Topic:
Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Mej
Please Search Seq ID No: 10
NA 2649
No Abstract please.
No size limits
Thurs.

STAFF USE ONLY

Searcher: _____

Searcher Phone #: _____

Searcher Location: _____

Date Searcher Picked Up: 5/20/05

Date Completed: 5/23/05

Searcher Prep & Review Time: _____

Online Time: _____

Type of Search

1 NA Sequence (#)

AA Sequence (#)

Structure (#)

Bibliographic

Litigation

Fulltext

Other

Vendors and cost where applicable

STN Dialog

Questel/Orbit Lexis/Nexis

Westlaw WWW/Internet

03P In-house sequence systems

Commercial Oligomer Score/Length
Interference SPDI Encode/Transl
Other (specify)

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 22, 2005, 05:00:17 ; Search time 8884 Seconds
(without alignments)
12172.472 Million cell updates/sec

Title: US-09-486-757-10
Perfect score: 2649
Sequence: 1 cggcagcagctttagtat.....tttgagagaaaaaaaaa 2649

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapept 1.0

Searched: 45554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters: 91109746

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Pending Patents_NA_Main:*

- 1: /cgn2_6/ptodata/1/pna/PCTUS1_COMB.seq.*
- 2: /cgn2_6/ptodata/1/pna/PCTUS2_COMB.seq.*
- 3: /cgn2_6/ptodata/1/pna/PCTUS3_COMB.seq.*
- 4: /cgn2_6/ptodata/1/pna/US06_COMB.seq.*
- 5: /cgn2_6/ptodata/1/pna/US07_COMB.seq.*
- 6: /cgn2_6/ptodata/1/pna/US08_COMB.seq.*
- 7: /cgn2_6/ptodata/1/pna/US081_COMB.seq.*
- 8: /cgn2_6/ptodata/1/pna/US082_COMB.seq.*
- 9: /cgn2_6/ptodata/1/pna/US083_COMB.seq.*
- 10: /cgn2_6/ptodata/1/pna/US084_COMB.seq.*
- 11: /cgn2_6/ptodata/1/pna/US085_COMB.seq.*
- 12: /cgn2_6/ptodata/1/pna/US086_COMB.seq.*
- 13: /cgn2_6/ptodata/1/pna/US087_COMB.seq.*
- 14: /cgn2_6/ptodata/1/pna/US088_COMB.seq.*
- 15: /cgn2_6/ptodata/1/pna/US089_COMB.seq.*
- 16: /cgn2_6/ptodata/1/pna/US090_COMB.seq.*
- 17: /cgn2_6/ptodata/1/pna/US091_COMB.seq.*
- 18: /cgn2_6/ptodata/1/pna/US092A_COMB.seq.*
- 19: /cgn2_6/ptodata/1/pna/US092B_COMB.seq.*
- 20: /cgn2_6/ptodata/1/pna/US093A_COMB.seq.*
- 21: /cgn2_6/ptodata/1/pna/US093B_COMB.seq.*
- 22: /cgn2_6/ptodata/1/pna/US094_COMB.seq.*
- 23: /cgn2_6/ptodata/1/pna/US095A_COMB.seq.*
- 24: /cgn2_6/ptodata/1/pna/US095B_COMB.seq.*
- 25: /cgn2_6/ptodata/1/pna/US095C_COMB.seq.*
- 26: /cgn2_6/ptodata/1/pna/US095D_COMB.seq.*
- 27: /cgn2_6/ptodata/1/pna/US096A_COMB.seq.*
- 28: /cgn2_6/ptodata/1/pna/US096B_COMB.seq.*
- 29: /cgn2_6/ptodata/1/pna/US096C_COMB.seq.*
- 30: /cgn2_6/ptodata/1/pna/US096D_COMB.seq.*
- 31: /cgn2_6/ptodata/1/pna/US096E_COMB.seq.*
- 32: /cgn2_6/ptodata/1/pna/US097A_COMB.seq.*
- 33: /cgn2_6/ptodata/1/pna/US097B_COMB.seq.*
- 34: /cgn2_6/ptodata/1/pna/US097C_COMB.seq.*
- 35: /cgn2_6/ptodata/1/pna/US098A_COMB.seq.*
- 36: /cgn2_6/ptodata/1/pna/US098B_COMB.seq.*
- 37: /cgn2_6/ptodata/1/pna/US098C_COMB.seq.*
- 38: /cgn2_6/ptodata/1/pna/US098D_COMB.seq.*
- 39: /cgn2_6/ptodata/1/pna/US099A_COMB.seq.*
- 40: /cgn2_6/ptodata/1/pna/US099B_COMB.seq.*
- 41: /cgn2_6/ptodata/1/pna/US099C_COMB.seq.*
- 42: /cgn2_6/ptodata/1/pna/US099D_COMB.seq.*
- 43: /cgn2_6/ptodata/1/pna/US099E_COMB.seq.*

- 44: /cgn2_6/ptodata/1/pna/US099F_COMB.seq.*
- 45: /cgn2_6/ptodata/1/pna/US099G_COMB.seq.*
- 46: /cgn2_6/ptodata/1/pna/US100A_COMB.seq.*
- 47: /cgn2_6/ptodata/1/pna/US100B_COMB.seq.*
- 48: /cgn2_6/ptodata/1/pna/US101A_COMB.seq.*
- 49: /cgn2_6/ptodata/1/pna/US101B_COMB.seq.*
- 50: /cgn2_6/ptodata/1/pna/US102A_COMB.seq.*
- 51: /cgn2_6/ptodata/1/pna/US102B_COMB.seq.*
- 52: /cgn2_6/ptodata/1/pna/US103A_COMB.seq.*
- 53: /cgn2_6/ptodata/1/pna/US103B_COMB.seq.*
- 54: /cgn2_6/ptodata/1/pna/US104A_COMB.seq.*
- 55: /cgn2_6/ptodata/1/pna/US104B_COMB.seq.*
- 56: /cgn2_6/ptodata/1/pna/US105A_COMB.seq.*
- 57: /cgn2_6/ptodata/1/pna/US105B_COMB.seq.*
- 58: /cgn2_6/ptodata/1/pna/US106A_COMB.seq.*
- 59: /cgn2_6/ptodata/1/pna/US107A_COMB.seq.*
- 60: /cgn2_6/ptodata/1/pna/US107B_COMB.seq.*
- 61: /cgn2_6/ptodata/1/pna/US107C_COMB.seq.*
- 62: /cgn2_6/ptodata/1/pna/US107D_COMB.seq.*
- 63: /cgn2_6/ptodata/1/pna/US108A_COMB.seq.*
- 64: /cgn2_6/ptodata/1/pna/US108B_COMB.seq.*
- 65: /cgn2_6/ptodata/1/pna/US109A_COMB.seq.*
- 66: /cgn2_6/ptodata/1/pna/US109B_COMB.seq.*
- 67: /cgn2_6/ptodata/1/pna/US109C_COMB.seq.*
- 68: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
- 69: /cgn2_6/ptodata/1/pna/US600_COMB.seq.*
- 70: /cgn2_6/ptodata/1/pna/US6001_COMB.seq.*
- 71: /cgn2_6/ptodata/1/pna/US6002_COMB.seq.*
- 72: /cgn2_6/ptodata/1/pna/US6003_COMB.seq.*
- 73: /cgn2_6/ptodata/1/pna/US6004_COMB.seq.*
- 74: /cgn2_6/ptodata/1/pna/US6005_COMB.seq.*
- 75: /cgn2_6/ptodata/1/pna/US6006_COMB.seq.*
- 76: /cgn2_6/ptodata/1/pna/US6007_COMB.seq.*
- 77: /cgn2_6/ptodata/1/pna/US6008_COMB.seq.*
- 78: /cgn2_6/ptodata/1/pna/US6009_COMB.seq.*
- 79: /cgn2_6/ptodata/1/pna/US6010_COMB.seq.*
- 80: /cgn2_6/ptodata/1/pna/US6011_COMB.seq.*
- 81: /cgn2_6/ptodata/1/pna/US6012_COMB.seq.*
- 82: /cgn2_6/ptodata/1/pna/US6013_COMB.seq.*
- 83: /cgn2_6/ptodata/1/pna/US6014_COMB.seq.*
- 84: /cgn2_6/ptodata/1/pna/US6015_COMB.seq.*
- 85: /cgn2_6/ptodata/1/pna/US6016_COMB.seq.*
- 86: /cgn2_6/ptodata/1/pna/US6017_COMB.seq.*
- 87: /cgn2_6/ptodata/1/pna/US6018_COMB.seq.*
- 88: /cgn2_6/ptodata/1/pna/US6019_COMB.seq.*
- 89: /cgn2_6/ptodata/1/pna/US6020_COMB.seq.*
- 90: /cgn2_6/ptodata/1/pna/US6021_COMB.seq.*
- 91: /cgn2_6/ptodata/1/pna/US6022_COMB.seq.*
- 92: /cgn2_6/ptodata/1/pna/US6023A_COMB.seq.*
- 93: /cgn2_6/ptodata/1/pna/US6023B_COMB.seq.*
- 94: /cgn2_6/ptodata/1/pna/US6024_COMB.seq.*
- 95: /cgn2_6/ptodata/1/pna/US6025_COMB.seq.*
- 96: /cgn2_6/ptodata/1/pna/US6026_COMB.seq.*
- 97: /cgn2_6/ptodata/1/pna/US6027_COMB.seq.*
- 98: /cgn2_6/ptodata/1/pna/US6028_COMB.seq.*
- 99: /cgn2_6/ptodata/1/pna/US6029_COMB.seq.*
- 100: /cgn2_6/ptodata/1/pna/US6030_COMB.seq.*
- 101: /cgn2_6/ptodata/1/pna/US6031_COMB.seq.*
- 102: /cgn2_6/ptodata/1/pna/US6032_COMB.seq.*
- 103: /cgn2_6/ptodata/1/pna/US6033_COMB.seq.*
- 104: /cgn2_6/ptodata/1/pna/US6034_COMB.seq.*
- 105: /cgn2_6/ptodata/1/pna/US6035_COMB.seq.*
- 106: /cgn2_6/ptodata/1/pna/US6036_COMB.seq.*
- 107: /cgn2_6/ptodata/1/pna/US6037_COMB.seq.*
- 108: /cgn2_6/ptodata/1/pna/US6038_COMB.seq.*
- 109: /cgn2_6/ptodata/1/pna/US6039_COMB.seq.*
- 110: /cgn2_6/ptodata/1/pna/US6040_COMB.seq.*
- 111: /cgn2_6/ptodata/1/pna/US6041_COMB.seq.*
- 112: /cgn2_6/ptodata/1/pna/US6042_COMB.seq.*
- 113: /cgn2_6/ptodata/1/pna/US6043_COMB.seq.*
- 114: /cgn2_6/ptodata/1/pna/US6044_COMB.seq.*
- 115: /cgn2_6/ptodata/1/pna/US6045_COMB.seq.*
- 116: /cgn2_6/ptodata/1/pna/US6046_COMB.seq.*

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OM nucleic - nucleic search, using sw model

Run on: May 22, 2005, 05:22:02 ; Search time 760 Seconds

(without alignments)
7754.887 Million cell updates/sec

Title: US-09-486-757-10

Perfect score: 2649
Sequence: 1 cggcagcagctcttagtcat.....tttgagaaaaaaaaaaaa 2649

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 11689648 seqs, 1112441377 residues

Total number of hits satisfying chosen parameters: 23379296

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents NA New:*

- 1: /cgn2_6/prodata/1/pna/PCT_NEW_COMB.seq:*
- 2: /cgn2_6/prodata/1/pna/PCT_NEW_COMB.seq2:*
- 3: /cgn2_6/prodata/1/pna/US06_NEW_COMB.seq:*
- 4: /cgn2_6/prodata/1/pna/US07_NEW_COMB.seq:*
- 5: /cgn2_6/prodata/1/pna/US08_NEW_COMB.seq:*
- 6: /cgn2_6/prodata/1/pna/US09_NEW_COMB.seq:*
- 7: /cgn2_6/prodata/1/pna/US10_NEW_COMB.seq:*
- 8: /cgn2_6/prodata/1/pna/US10_NEW_COMB.seq2:*
- 9: /cgn2_6/prodata/1/pna/US10_NEW_COMB.seq3:*
- 10: /cgn2_6/prodata/1/pna/US10_NEW_COMB.seq4:*
- 11: /cgn2_6/prodata/1/pna/US11_NEW_COMB.seq:*
- 12: /cgn2_6/prodata/1/pna/US11_NEW_COMB.seq2:*
- 13: /cgn2_6/prodata/1/pna/US11_NEW_COMB.seq3:*
- 14: /cgn2_6/prodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | nd |
|------------|-------|-------------|--------|----|
| | | | | |

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OM nucleic - nucleic search, using sw model

Run on: May 22, 2005, 08:25:35 ; Search time 1432 Seconds

(without alignments)
11343.938 Million cell updates/sec

Title: US-09-486-757-10

Perfect score: 2649
Sequence: 1 cggcagcagctgtctgtat.....tttggagaaaaa 2649

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5695437 seqs, 306160638 residues

Total number of hits satisfying chosen parameters: 11390874

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | ID | Description |
|------------|-------|--------------------|-------|-------------|
| ----- | ----- | ----- | ----- | ----- |

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OM nucleic - nucleic search, using sw model

Run on: May 22, 2005, 04:40:28 ; Search time 455 Seconds
(without alignments)
9526.367 Million cell updates/sec

Title: US-09-486-757-10

Perfect score: 2649
Sequence: 1 cggcagcagctctgtat.....tttgagaaaaaaaaaaaa 2649

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 81818359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_MA:*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| ----- | | | | | |

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OM nucleic - nucleic search, using sw model

Run on: May 22, 2005, 00:44:41 ; Search time 1305 Seconds
(without alignments)
12016.394 Million cell updates/sec

Title: US-09-486-757-10

Perfect score: 2649
Sequence: 1 CGGCACGAGCTCTAGTAT.....TTCTGAGAAAAA 2649

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match length DB | ID | Description |
|---------------|-------|--------------------------|-------|-------------|
| ----- | ----- | ----- | ----- | ----- |

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OM nucleic - nucleic search, using sw model

Run on: May 22, 2005, 02:29:27 ; Search time 11003 Seconds
(without alignments)
11665.715 Million cell updates/sec

Title: US-09-486-757-10

Perfect score: 2649

Sequence: 1 cggcagcagctctgtctat.....tttctggaataaaaaaa 2649

Scoring table: IDENTITY_NTC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing filter 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sgs:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|--------------------|
| 1 | 2645.8 | 99.9 | 2650 | 8 | PSU67185 |
| 2 | 1126.4 | 42.5 | 2498 | 8 | AF302496 Hybrid po |
| 3 | 1104.8 | 41.7 | 2617 | 8 | VIRNADPH4 |
| 4 | 1094.8 | 41.3 | 2641 | 8 | VSNFR |
| 5 | 1086.2 | 41.0 | 2633 | 8 | AY170374 |
| 6 | 1071.4 | 40.5 | 2693 | 8 | AB086169 |
| 7 | 1061.4 | 40.1 | 2685 | 8 | BT013756 |
| 8 | 1039 | 39.2 | 2079 | 8 | AY586976 |
| 9 | 1030.8 | 38.9 | 2059 | 8 | AY520902 |
| 10 | 997.2 | 37.6 | 2340 | 8 | AY054688 |
| 11 | 994.6 | 37.5 | 2079 | 8 | BT008426 |
| 12 | 987.6 | 37.3 | 2199 | 8 | ATATRIC |
| 13 | 985 | 37.2 | 2114 | 6 | A75959 |
| 14 | 969.8 | 36.6 | 2561 | 8 | ECU67186 |
| 15 | 918.6 | 34.7 | 2493 | 8 | AF302497 |
| 16 | 912.6 | 34.5 | 2631 | 8 | PM14CPR |
| 17 | 911.2 | 34.4 | 2610 | 8 | AF302498 |
| 18 | 895.4 | 33.8 | 2136 | 6 | AX506108 |
| 19 | 895.4 | 33.8 | 2136 | 6 | AX651759 |

| | | | | | | |
|----|-------|------|------|---|-----------|---------------------|
| 20 | 895.4 | 33.8 | 2136 | 8 | AF325101 | AF325101 Arabidops |
| 21 | 875.2 | 33.0 | 2556 | 8 | AF024635 | AF024635 Petrosell |
| 22 | 875 | 33.0 | 2290 | 8 | ATATRM | X65017 A.thaliana |
| 23 | 875 | 33.0 | 2423 | 6 | A75961 | A75961 Sequence 3 |
| 24 | 874 | 33.0 | 2466 | 8 | AF024634 | AF024634 Petrosell |
| 25 | 873.6 | 33.0 | 2618 | 8 | CRCRPA | X69791 C.roseus cp |
| 26 | 867.4 | 32.7 | 2333 | 8 | AF123610 | AF123610 Trifolium |
| 27 | 864.8 | 32.6 | 2472 | 8 | AY532374 | AY532374 Armi maju |
| 28 | 862.4 | 32.6 | 2545 | 8 | AF002698 | AF002698 Pisum sat. |
| 29 | 859.8 | 32.5 | 2412 | 6 | A75963 | A75963 Sequence 5 |
| 30 | 852.6 | 32.2 | 2482 | 8 | AK102060 | AK102060 Oryza sat |
| 31 | 850 | 32.1 | 2420 | 8 | TAB303373 | AJ303373 Trifolium |
| 32 | 808.4 | 30.5 | 2298 | 8 | AK068915 | AK068915 Oryza sat |
| 33 | 808.4 | 30.5 | 2298 | 8 | AK099083 | AK099083 Oryza sat |
| 34 | 807.6 | 30.5 | 1863 | 6 | AR205034 | AR205034 Sequence |
| 35 | 807.6 | 30.5 | 1863 | 6 | AR282641 | AR282641 Sequence |
| 36 | 807.6 | 30.5 | 1863 | 6 | AX082548 | AX082548 Sequence |
| 37 | 807.6 | 30.5 | 1863 | 6 | AX370663 | AX370663 Sequence |
| 38 | 807.6 | 30.5 | 1863 | 8 | HTU2NFR | 226550 H.tuberosus |
| 39 | 659.2 | 24.9 | 1539 | 8 | HTU2NFR | 226550 H.tuberosus |
| 40 | 606.6 | 22.9 | 1714 | 8 | AK101320 | AK101320 Oryza sat |
| 41 | 586.4 | 22.1 | 2016 | 6 | AK654074 | AK654074 Sequence |
| 42 | 569.6 | 21.5 | 2312 | 8 | AF367288 | AF367288 Arabidops |
| 43 | 473.6 | 17.9 | 1023 | 8 | AY059162 | AY059162 Arabidops |
| 44 | 295.8 | 11.2 | 715 | 8 | HTU58629 | U58629 Helianthus |
| 45 | 282.4 | 10.7 | 1078 | 8 | PAB132538 | AJ132538 Picea abi |

ALIGNMENTS

| | | | | | |
|---|--|------------|------|--------|-----------------|
| RESULT 1 | PSU67185 | 2650 bp | mRNA | linear | PLN 06-MAR-1998 |
| LOCUS | PSU67185 | | | | |
| DEFINITION | Papaver somniferum NADPH:ferredoxin oxidoreductase mRNA, | | | | |
| ACCESSION | U67185 | | | | |
| VERSION | U67185.1 | GI:2580496 | | | |
| KEYWORDS | | | | | |
| SOURCE | Papaver somniferum (opium poppy) | | | | |
| ORGANISM | Papaver somniferum | | | | |
| REFERENCE | 1 (bases 1 to 2650) | | | | |
| AUTHORS | Rosco, A., Pauli, H.H., Priemer, W. and Kutchan, T.M. | | | | |
| TITLE | Cloning and heterologous expression of NADPH-cytochrome P450 | | | | |
| JOURNAL | Arch. Biochem. Biophys. 348 (2), 369-377 (1997) | | | | |
| MEDLINE | 9809363 | | | | |
| PubMed | 9434750 | | | | |
| REFERENCE | 2 (bases 1 to 2650) | | | | |
| AUTHORS | Rosco, A. and Kutchan, T.M. | | | | |
| TITLE | Direct Substitution | | | | |
| JOURNAL | Submitted (19-AUG-1996) Laboratorium fuer Molekulare Biologie, | | | | |
| University of Munich, Karlstrasse 29, Munich 80333, Germany | | | | | |
| Location/Qualifiers | | | | | |
| FEATURES | 1..2650 | | | | |
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| | heme-thiolate-dependent monooxygenases and oxidases; | | | | |
| | reduces cytochrome c" | | | | |
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